

OM nucleic - nucleic search, using sw model

Run on: July 7, 2004, 17:46:47 ; Search time 3204.75 seconds  
(without alignments)  
16080.756 Million cell updates/sec

Title: US-10-018-786-3  
Perfect score: 1189  
Sequence: 1 aaattgcacaggtgatgc.....gcttgtgacacagtggaag 1189

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- 1: gb\_ba.\*
- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_fo.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_om.\*
- 21: em\_or.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
- 24: em\_ph.\*
- 25: em\_pl.\*
- 26: em\_ro.\*
- 27: em\_sts.\*

- 28: em\_un.\*
- 29: em\_vi.\*
- 30: em\_htg\_hum.\*
- 31: em\_htg\_inv.\*
- 32: em\_htg\_other.\*
- 33: em\_htg\_mus.\*
- 34: em\_htg\_pln.\*
- 35: em\_htg\_rnd.\*
- 36: em\_htg\_mam.\*
- 37: em\_htg\_vrt.\*
- 38: em\_sy.\*
- 39: em\_htg\_hum.\*
- 40: em\_htg\_mus.\*
- 41: em\_htg\_other.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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c	4	944.8	79.5	5071	1	AF320050	AF320050 Xanthomon
c	5	944.8	79.5	6454	1	AY139029S2	AY139029 Xanthomon
c	6	944.8	79.5	19304	1	AB045311	AB045311 Xanthomon
c	7	944.8	79.5	23514	1	AY205561	AY205561 Xanthomon
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ALIGNMENTS

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DEFINITION AX061802  
ACCESSION AX061802  
VERSION AX061802.1 GI:12539892  
KEYWORDS Xanthomonas campestris  
SOURCE Xanthomonas campestris  
ORGANISM Xanthomonas campestris

REFERENCE 1  
AUTHORS Plerard,J., Simon,J.L. and Chevallereau,P.  
TITLE Avirulent xanthomonas-campestris strains producing xanthan  
JOURNAL Patent: WO 0078967-A 3 28-DEC-2000;  
RHODIA CHIMIE (FR)

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 VERSION AE012222.1 GI:21112273  
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 ORGANISM Xanthomonas campestris pv. campestris str. ATCC 33913  
 Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Xanthomonas.

REFERENCE  
 AUTHORS  
 1 (bases 1 to 11629)  
 da Silva,A.C.R., Ferro,J.A., Reinach,F.C., Farah,C.S., Furlan,L.R., Quaggio,R.B., Monteiro-Vitorello,C.B., Van Sluys,M.A., Almeida Jr.,N.F., Alves,L.M.C., do Amaral,A.M., Bertolini,M.C., Camargo,L.E.A., Camarotte,G., Cannavan,F., Cardozo,J., Chambergo,F., Ciapina,L.P., Ciccarelli,R.M.B., Coutinho,L.L., Cursino-Santos,J.R., El-Dorry,H., Faria,J.B., Ferreira,A.J.S., Ferreira,R.C.C., Ferro,M.I.T., Fornighieri,E.F., Franco,M.C., Greggio,C.C., Gruber,A., Katsuyama,A.M., Kishi,L.T., Leite Jr.,R.P., Lemos,E.G.M., Lemos,M.V.F., Locali,E.C., Machado,M.A., Madalira,A.M.B.N., Martinez-Rossi,N.M., Martins,E.C., Meidanis,J., Menck,C.F.M., Miyaki,C.Y., Moon,D.H., Moreira,L.M., Novo,M.T.M., Okura,V.K., Oliveira,M.C., Oliveira,V.R., Pereira Jr.,H.A., Rossi,A., Sena,J.A.D., Silva,C., de Souza,R.F., Spinola,L.A.F., Takita,M.A., Tamura,R.E., Teixeira,E.C., Tezza,R.I.D., Trindade dos Santos,M., Truffi,D., Tsai,S.M., White,F.F., Setubal,J.C. and Kitajima,J.P.  
 Comparison of the genomes of two Xanthomonas pathogens with differing host specificities  
 Nature 417 (6887), 459-463 (2002)

TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED  
 22022145  
 12024217

REFERENCE  
 AUTHORS  
 2 (bases 1 to 11629)  
 da Silva,A.C.R., Ferro,J.A., Reinach,F.C., Farah,C.S., Furlan,L.R., Quaggio,R.B., Monteiro-Vitorello,C.B., Van Sluys,M.A., Almeida Jr.,N.F., Alves,L.M.C., do Amaral,A.M., Bertolini,M.C., Camargo,L.E.A., Camarotte,G., Cannavan,F., Cardozo,J., Chambergo,F., Ciapina,L.P., Ciccarelli,R.M.B., Coutinho,L.L., Cursino-Santos,J.R., El-Dorry,H., Faria,J.B., Ferreira,A.J.S., Ferreira,R.C.C., Ferro,M.I.T., Fornighieri,E.F., Franco,M.C., Greggio,C.C., Gruber,A., Katsuyama,A.M., Kishi,L.T., Leite Jr.,R.P., Lemos,E.G.M., Lemos,M.V.F., Locali,E.C., Machado,M.A., Madalira,A.M.B.N., Martinez-Rossi,N.M., Martins,E.C., Meidanis,J., Menck,C.F.M., Miyaki,C.Y., Moon,D.H., Moreira,L.M., Novo,M.T.M.,

Okura,V.K., Oliveira,M.C., Oliveira,V.R., Pereira Jr.,H.A., Rossi,A., Sena,J.A.D., Silva,C., de Souza,R.F., Spinola,L.A.F., Takita,M.A., Tamura,R.E., Teixeira,E.C., Tezza,R.I.D., Trindade dos Santos,M., Truffi,D., Tsai,S.M., White,F.F., Setubal,J.C. and Kitajima,J.P.  
 Direct Submission  
 Submitted (28-NOV-2001) Departamento de Bioquímica, Universidade de Sao Paulo, Av. Prof. Lineu Prestes 748, Sao Paulo, SP 05508-900, Brazil

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Query Match 99.5%; Score 1183.2; DB 1; Length 11629;  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 7, 2004, 17:42:57 ; Search time 347.5 seconds  
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Perfect score: 1189  
Sequence: 1 aaattctgaaggatgatgc.....gcttgacaccaggtgaaa 1189

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 337363 seqs, 2124099041 residues  
Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_29Jan04:\*

- 1: geneseqn1980s:\*
- 2: geneseqn1990s:\*
- 3: geneseqn2000s:\*
- 4: geneseqn2001as:\*
- 5: geneseqn2001bs:\*
- 6: geneseqn2002as:\*
- 7: geneseqn2003as:\*
- 8: geneseqn2003bs:\*
- 9: geneseqn2003cs:\*
- 10: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1189	100.0	1189	5 ABL57891	ABL57891 Partial h
c 2	203.6	17.1	1218	7 ACA26203	ACA26203 Prokaryot
c 3	142	11.9	2100	3 AAA64849	AAA64849 Bordetell
c 4	142	11.9	35026	3 AAA64890	AAA64890 Bordetell
5	137.6	11.6	5678	6 AEN86172	AEN86172 A. salmon
6	130.8	11.0	2103	3 AAZ45563	AAZ45563 Nucleotid
c 7	130.8	11.0	13500	3 AAZ45562	AAZ45562 Nucleotid

c 8	120.8	10.2	1899	7 ACA26479	ACA26479 Prokaryot
9	111.4	9.4	2118	7 ACF71579	ACF71579 Photobab
c 10	111.4	9.4	110000	7 ACF67367	Continuation (48 o
c 11	111.4	9.4	110000	7 ACF65388	ACF65388 Photobab
c 12	103.4	8.7	2181	7 ACA26011	ACA26011 Prokaryot
c 13	98	8.2	34720	2 AAV30458	Continuation (6 of
14	98	8.2	36165	2 AAV30459	Continuation (6 of
15	95.2	8.0	2124	7 ABX94896	ABX94896 P. aurogl
16	89.4	7.5	110000	2 AAZ01425	Continuation (4 of
17	88.8	7.5	849	5 AAS70994	AAS70994 DNA encod
18	87.8	7.4	2127	9 ADD43765	ADD43765 Chlamydia
c 19	86.6	7.3	609	5 AAS73035	AAS73035 DNA encod
20	85.4	7.2	2704	5 AAS73037	AAS73037 DNA encod
21	81	6.8	2058	2 AAQ34562	AAQ34562 Sequence
22	81	6.8	2058	7 ACA19671	ACA19671 Prokaryot
c 23	80.2	6.7	958	6 ABK74562	ABK74562 Bacillus
c 24	79.4	6.7	2310	5 AAS92707	AAS92707 DNA encod
c 25	72.2	6.1	2082	7 ACF68505	ACF68505 Photobab
c 26	72.2	6.1	110000	7 ACF67367	Continuation (13 o
27	72.2	6.1	182624	7 ACF65379	ACF65379 Photobab
28	71.8	6.0	2350	3 AAZ61505	AAZ61505 DNA encod
29	71.8	6.0	110000	2 AAX91990	Continuation (4 of
c 30	71.8	6.0	273254	3 AAC81914	AAC81914 Chlamydia
c 31	71.4	6.0	43360	8 ACD19193	ACD19193 E. coli o
c 32	71.4	6.0	43450	9 ADC00771	ADC00771 Enterobac
c 33	71.4	6.0	45325	8 ACD19247	ACD19247 E. coli o
c 34	70.6	5.9	13417	2 AAT09224	AAT09224 Partial s
35	70	5.9	660	6 ABX66374	ABX66374 Helicobac
36	70	5.9	1024	6 ABX66703	ABX66703 Helicobac
37	70	5.9	2202	4 AAF25596	AAF25596 H. pylori
c 38	67.4	5.7	16943	9 ADC01147	ADC01147 Enterobac
c 39	67.4	5.7	16950	8 ACD19153	ACD19153 E. coli o
40	64.4	5.4	500	6 ABK78960	ABK78960 Bacillus
41	63.6	5.3	2501	2 AAT62336	AAT62336 Helicobac
42	62.6	5.3	726	6 ABQ19426	ABQ19426 oligonuel
c 43	62.6	5.3	726	6 ABQ19427	ABQ19427 oligonuel
44	62.2	5.2	695	4 AAF25644	AAF25644 H. pylori
45	62	5.2	915	6 ABK74570	ABK74570 Bacillus

#### ALIGNMENTS

RESULT 1  
ABL57891  
ID ABL57891 standard; DNA; 1189 BP.

XX AC ABL57891;  
XX AC ABL57891;  
DT 11-SEP-2003 (revised)  
DT 04-JUL-2002 (first entry)  
XX  
DE Partial hypersensitive reaction and pathogenicity, hrpC2 gene.  
XX  
KW Hypersensitive reaction and pathogenicity; hrpC2; exo-polysaccharide;  
KW xanthan gum; gene; ds.  
XX

OS Xanthomonas campestris; pv vesicatoria.

PN WO200078967-A1.

XX 28-DEC-2000.

XX 21-JUN-2000; 2000WO-FR001725.

XX 22-JUN-1999; 99FR-00007963.

XX (RHOD ) RHODIA CHIM.

XX Pierrard J, Simon J, Chevallereau P;

XX WPI; 2001-102725/11.

XX New Xanthomonas campestris bacteria strains for use in production of exo-  
PT polysaccharides are made non-virulent by inactivation of at least one  
PT virulence gene.

XX Claim 17; Page 25-26; 33pp; French.

XX The present invention relates to new Xanthomonas campestris bacteria  
CC strains made non-virulent by inactivation of at least one virulence gene  
CC but which have retained the capacity to produce exo-polysaccharides  
CC (preferably xanthan gum). One such virulence gene deleted to produce the  
CC bacterial strains was the hrp2 gene (Hypersensitive Reaction and  
CC Pathogenicity). The hrp genes are essential for pathogenicity in plants.  
CC The present sequence is a partial sequence of the hrpC2, used in an  
CC example from the invention. (Updated on 11-SEP-2003 to standardise OS  
CC field)

XX Sequence 1189 BP; 226 A; 366 C; 392 G; 205 T; 0 U; 0 Other;

Query Match 100.0%; Score 1189; DB 5; Length 1189;  
Best Local Similarity 100.0%; Pred. No. 8.3e-250;  
Matches 1189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 A A A T T C G T C A A G G G T G A T G C A T C G C G G C C T G G T G A T C A C C A T G G T C A A C A T C T T G G G C 60  
DB 1 A A A T T C G T C A A G G G T G A T G C A T C G C G G C C T G G T G A T C A C C A T G G T C A A C A T C T T G G G C 60  
QY 61 G G C A T C G T G G T A G G G T G A C C T A C C A G G C A T G A G C G G G G G A G G C G G C C A C G G C T T 120  
DB 61 G G C A T C G T G G T A G G G T G A C C T A C C A G G C A T G A G C G G G G G A G G C G G C C A C G G C T T 120  
QY 121 G C A T C C T G T C G G T A G G C A T G C G A T G T G C A G A T C G C T C G T G C T G A T C T C G G T G 180  
DB 121 G C A T C C T G T C G G T A G G C A T G C G A T G T G C G A T G T G C G A T G C C T C G C T G C T G A T C T C G G T G 180  
QY 181 G C G G C G G G C G T C A T G A T C A C C C C G G T C G C C A A C G A A G A T G A A A C C A A G A T C A G T C G C T C 240  
DB 181 G C G G C G G G C G T C A T G A T C A C C C C G G T C G C C A A C G A A G A T G A A A C C A A G A T C A G T C G C T C 240  
QY 241 G G G C T C G A C A T C G G C C G C A C T C A C A G C A A C G A C G T G C C T T G A T G C A G C G G A G T G 300  
DB 241 G G G C T C G A C A T C G G C C G C A C T C A C A G C A A C G A C G T G C C T T G A T G C A G C G G A G T G 300

QY 1141 CTGGCGTGGCCACGGAGCAGGCGCAATCAGCTTGTGACGAGGTGGAAA 1189  
|||||  
Db 1141 CTGGCGTGGCCACGGAGCAGGCGCAATCAGCTTGTGACGAGGTGGAAA 1189  
|||||

Search completed: July 7, 2004, 21:07:43  
Job time : 352.5 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 7, 2004, 20:18:17 ; Search time 2289.2 Seconds  
(without alignments)  
15510.269 Million cell updates/sec

Title: US-10-018-786-3  
Perfect score: 1189  
Sequence: 1 aaattgtcaagggtgatgc.....gcttgcgaccagtgga 1189

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:  
1: em\_estba:  
2: em\_esthum:  
3: em\_estin:  
4: em\_estmu:  
5: em\_estov:  
6: em\_estpl:  
7: em\_estro:  
8: em\_htc:  
9: gb\_est1:  
10: gb\_est2:  
11: gb\_htc:  
12: gb\_est3:  
13: gb\_est4:  
14: gb\_est5:  
15: em\_estfun:  
16: em\_estom:  
17: em\_gss\_hum:  
18: em\_gss\_inv:  
19: em\_gss\_pln:  
20: em\_gss\_vrt:  
21: em\_gss\_fun:  
22: em\_gss\_mam:  
23: em\_gss\_mus:  
24: em\_gss\_pro:  
25: em\_gss\_rod:  
26: em\_gss\_phg:  
27: em\_gss\_vrl:

28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			ID	Description	
	score	Match	Length			
1	145.6	12.2	1259	28	B2555432 paes1-60	
c	2	104.6	8.8	899	28	B2578201 msh2_5747
c	3	103.8	8.7	707	28	BH614295 1C22/2B8
c	4	103.8	8.7	707	28	BH614489 2B8 Contl
c	5	100.6	8.5	1336	28	B2554711 paes1-60
c	6	97.4	8.2	1361	28	B2575790 msh2_4628
c	7	79.6	6.7	673	28	B2548588 paes1-60
c	8	76.4	6.4	446	13	C07126 C07126 Rat
c	9	69.6	5.9	787	28	BH795460 04B01LL10
c	10	66.6	5.6	1129	28	B2558715 paes1-60
c	11	66.4	5.6	541	28	A2303060 GSSB-r200
c	12	62.6	5.3	1446	28	BH614290 1C22/2B8
c	13	62.6	5.3	1446	28	BH614482 2B8 Contl
c	14	57.6	4.8	414	14	CF143739 UI-HF-BPO
c	15	55.4	4.7	925	29	CNS0091P
c	16	55	4.6	925	29	CNS0091P
c	17	51.8	4.4	540	28	B2894800 Hg3_0183
c	18	48.6	4.1	762	29	CNS01XFI
c	19	48.2	4.1	746	28	B2561680 paes2-164
c	20	48.2	4.1	935	29	CNS006XK
c	21	47.8	4.0	790	13	BW263485
c	22	47.8	4.0	834	10	BF267459
c	23	47.6	4.0	1201	13	BX356664
c	24	47.4	4.0	538	29	CC663357
c	25	47.4	4.0	783	28	BZ641592
c	26	47.4	4.0	827	29	CC717827
c	27	47	4.0	629	13	BW222739
c	28	46.8	3.9	548	6	AL814243
c	29	46.8	3.9	567	6	AL815397
c	30	46.8	3.9	661	12	B1960553
c	31	46.8	3.9	1100	29	CNS016KD
c	32	46.6	3.9	600	28	BZ896342
c	33	46.6	3.9	696	14	CA289460
c	34	46.6	3.9	766	13	BW101474
c	35	46.4	3.9	622	12	BM441961
c	36	46.4	3.9	1100	29	CNS016KD
c	37	46.2	3.9	580	14	CB878329
c	38	46.2	3.9	601	28	AY079696
c	39	46	3.9	844	29	CNS0052P
c	40	46	3.9	877	29	CG347796
c	41	45.8	3.8	529	14	CD232008
c	42	45.6	3.8	745	29	CC846671
c	43	45.6	3.8	906	28	CC122201
c	44	45.4	3.8	654	13	CA040006
c	45	45.4	3.8	742	14	CF774722